



Seq_listing_US_korrigiert141102.txt
SEQUENCE LISTING

<110> Forschungszentrum Juelich GmbH; Marina Vrlijc et al.

<120> Process for the microbial production of amino acids by boosted activity of export carriers

<130> 1

<140> US/09/105,117 PCT/DE96/02485

<141> 1998-06-17

<160> 5

<170> PatentIn Ver. 2.0

<210> 1

<211> 2374

<212> DNA

<213> Corynebacterium glutamicum

<220> (LysE)

<221> gene

<222> CDS (1016)..(1726)

<400> 1

ccatttgctg aagggtttac tctgcctggc ccaattcctg cgggcagaaga agtgaaaaac 60

cctgaacctt ttcagaagta actaaggccg caatccctcg attgctgcatt caacgacggc 120

gtctgtgagt ctagctagag atctagattc caggcgccat cgttgccaat acatcggtgt 180

gtcaatgggt atctcatcga ggaggatcac ttctcctgct ttttagcatgg gagcagctt 240

ggtttcggga agaagtcccc aaccaaggcc tcggcgaatt gcctcaccaa aacccccc 300

cgacgggaca atggatacgc gcctgcgccc cacaggacca tcgacgcgcc cgtccaggc 360

acggcttga agcacatctt tgggaccgaa gcgttaagacg ggcacatcgacg cccaatctt 420

tttcccatca accatgttagg catcccgaa tgagggggtt gcaatggcca agtggcgcat 480

ggttccaagt tctactactt cacatccgc cacgggatta gcttcacggg ttaccgctcc 540

taaaacatct ccacgcccga gcaaggataa tgtgtgcgct tcacatccca agcgcagcgt 600

gagcgttgct ccaccccaag aagctacctc gttgaacacg ggagggaaacc atgtggatag 660

cgaatctgcg ttgatggcga tggtaacgg gatttcagca aggcgtccag atagttgcgc 720

tttagttct gcttgcagca acaccatttt ccgcgtcgct tgcacaagga cttcacccgc 780

ttcggttgct ttggccgggtt gggtgcgca taccaacact cgacccacgt gatgctcgag 840

agctttaacg cgctgactca ccgcccgggg ggaaatggaa agggctaagg aggcgccttc 900

gaagctgcct tcacatga ttgagagcaa agtgtccagt tgaatgggt tcatgaagct 960

atattaaacc atgttaagaa ccaatcattt tacttaagta cttccatagg tcacg atg 1018

Met
1

Seq_Listing_US_korrigiert141102.txt

gtg atc atg gaa atc ttc att aca ggt ctg ctt ttg ggg gcc agt ctt 1066
 Val Ile Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser Leu
 5 10 15

tta ctg tcc atc gga ccg cag aat gta ctg gtg att aaa caa gga att 1114
 Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly Ile
 20 25 30

aag cgc gaa gga ctc att gcg gtt ctt ctc gtg tgt tta att tct gac 1162
 Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser Asp
 35 40 45

gtc ttt ttg ttc atc gcc ggc acc ttg ggc gtt gat ctt ttg tcc aat 1210
 Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser Asn
 50 55 60 65

gcc gcg ccg atc gtg ctc gat att atg cgc tgg ggt ggc atc gct tac 1258
 Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Ile Ala Tyr
 70 75 80

ctg tta tgg ttt gcc gtc atg gca gcg aaa gac gcc atg aca aac aag 1306
 Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn Lys
 85 90 95

gtg gaa gcg cca cag atc att gaa gaa aca gaa cca acc gtg ccc gat 1354
 Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro Asp
 100 105 110

gac acg cct ttg ggc ggt tcg gcg gtg gcc act gac acg cgc aac cgg 1402
 Asp Thr Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn Arg
 115 120 125

gtg cgg gtg gag gtg agc gtc gat aag cag cgg gtt tgg gta aag ccc 1450
 Val Arg Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys Pro
 130 135 140 145

atg ttg atg gca atc gtg ctg acc tgg ttg aac ccg aat gcg tat ttg 1498
 Met Leu Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr Leu
 150 155 160

gac gcg ttt gtg ttt atc ggc ggc gtc ggc gcg caa tac ggc gac acc 1546
 Asp Ala Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp Thr
 165 170 175

gga cgg tgg att ttc gcc gct ggc gcg ttc gcg gca agc ctg atc tgg 1594
 Gly Arg Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile Trp
 180 185 190

ttc ccg ctg gtg ggt ttc ggc gca gca gca ttg tca cgc ccg ctg tcc 1642
 Phe Pro Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu Ser
 195 200 205

agc ccc aag gtg tgg cgc tgg atc aac gtc gtc gtg gca gtt gtg atg 1690
 Ser Pro Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val Met
 210 215 220 225

acc gca ttg gcc atc aaa ctg atg ttg atg ggt tag ttttcgcggg 1736
 Thr Ala Leu Ala Ile Lys Leu Met Leu Met Gly
 230 235

ttttgaaatc ggtggccttc gcccaaatgt tgatgccggc gtcgtggaa atctcatcga 1796

Seq_listing_US_korrigiert141102.txt

tcgcctccaa ctcggcgtaa gaaaactcca agttgttag tgaatcaagg ctgtgtcca 1856
gctgctcaac tgacgaagca ccaatcaatg cactggtcac ggtatccgcg ccgtactctc 1916
cttgctcgcg cagcacccat gcaagcgcca tctgcgcaag tgactgcccg cgttcctggg 1976
cgatgtcatt gagcttgcgg accatatcaa tattgttac gttcaacatg ccctcagaca 2036
gggacttacc ctggctggcg cgggAACCT ctggaattcc atcgagatat ttgtccgtga 2096
gcagggccctg cgcaagtggt gagaaagcaa tgacgccaag accattgttgcagact 2156
gcaacaagtt ctcaccgtca tcgcccgggtt cctccaccca acgattaatg atgaaatagc 2216
ttggctgatg aatcagaagc gggcagccct cctccgccat gaactcagcc gcctccgctg 2276
tgagctctgg accgttagaa gaaataccca cgtaaagagc cttccagac gcaacaatgt 2336
cacgcaatgc gtacatggtt tcttccaaag gagtatct 2374

<210> 2
<211> 236
<212> PRT
<213> Corynebacterium glutamicum
<220> (LysE)

<400> 2
Met Val Ile Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser
1 5 10 15
Leu Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly
20 25 30
Ile Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser
35 40 45
Asp Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser
50 55 60
Asn Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala
65 70 75 80
Tyr Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn
85 90 95
Lys Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro
100 105 110
Asp Asp Thr Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn
115 120 125
Arg Val Arg Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys
130 135 140
Pro Met Leu Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr
145 150 155 160
Leu Asp Ala Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp
165 170 175

Thr Gly Arg Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile
 180 185 190
 Trp Phe Pro Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu
 195 200 205
 Ser Ser Pro Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val
 210 215 220
 Met Thr Ala Leu Ala Ile Lys Leu Met Leu Met Gly
 225 230 235

<210> 3
 <211> 2374
 <212> DNA
 <213> Corynebacterium glutamicum
 <220> (complement to <210> 1)
 <221> unsure
 <222>CDS (2)..(652)
 <223>orf3
 <220>
 <221>gene
 <222>CDS (1421)..(2293)
 <223>LysG

<400> 3
 a gat act cct ttg gaa gaa acc atg tac gca ttg cgt gac att gtt gcg 49
 Asp Thr Pro Leu Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile Val Ala
 1 5 10 15

tct gga aag gct ctt tac ttg ggt att tct tcc tac ggt cca gag ctc 97
 Ser Gly Lys Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu Leu
 20 25 30

aca gcg gag gcg gct gag ttc atg gcg gag gag ggc tgc ccg ctt ctg 145
 Thr Ala Glu Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu Leu
 35 40 45

att cat cag cca agc tat tcc atc att aat cgt tgg ttg gag gaa ccg 193
 Ile His Gln Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu Pro
 50 55 60

ggc gat gag ggt gag aac ttg ttg cag tca gct gcc aac aat ggt ctt 241
 Gly Asp Asp Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly Leu
 65 70 75 80

ggc gtc att gct ttc tca cca ctt gcg cag ggc ctg ctc acg gac aaa 289
 Gly Val Ile Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp Lys
 85 90 95

tat ctc gat gga att cca gag ggt tcc cgc gcc agc cag ggt aag tcc 337
 Tyr Leu Asp Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys Ser
 100 105 110

ctg tct gag ggc atg ttg aac gtc aac aat att gat atg gtc cgc aag 385
 Leu Ser Glu Gly Met Leu Asn Val Asn Asn Ile Asp Met Val Arg Lys
 115 120 125

ctc aat gac atc gcc cag gaa cgc ggg cag tca ctt gcg cag atg gcg 433

seq_listing_US_korrigiert141102.txt

Leu Asn Asp Ile Ala Gln Glu Arg Gly Gln Ser Leu Ala Gln Met Ala
 130 135 140
 ctt gca tgg gtg ctg cgc gag caa gga gag tac ggc gcg gat acc gtc 481
 Leu Ala Trp Val Leu Arg Glu Gln Gly Glu Tyr Gly Ala Asp Thr Val
 145 150 155 160
 acc agt gca ttg att ggt gct tcg tca gtt gag cag ctg gac aac agc 529
 Thr Ser Ala Leu Ile Gly Ala Ser Ser Val Glu Gln Leu Asp Asn Ser
 165 170 175
 ctt gat tca ctc aac aac ttg gag ttt tct gac gcc gag ttg gag gcg 577
 Leu Asp Ser Leu Asn Asn Leu Glu Phe Ser Asp Ala Glu Leu Glu Ala
 180 185 190
 atc gat gag att tcc cac gac gcc ggc atc aac att tgg gcg aag gcc 625
 Ile Asp Glu Ile Ser His Asp Ala Gly Ile Asn Ile Trp Ala Lys Ala
 195 200 205
 acc gat tcc aaa acc cgc gaa aac taa cccatcaaca tcagtttgc 672
 Thr Asp Ser Lys Thr Arg Glu Asn
 210 215
 ggccaatgcg gtcatcacaa ctgccacgac gacgttgatc cagccaca cttgggct 732
 ggacagcgg cgtgacaatg ctgctgcgc gaaacccacc agcggacc agatcaggct 792
 tgccgcgaac gcgcgcgg cgaaaatcca ccgtccggtg tcgccgtatt gcgcgcgc 852
 gccgcgata aacacaaacg cgtccaaata cgcattcggg ttcaaccagg tcagcacat 912
 tgccatcaac atgggcttta cccaaacccg ctgcttatcg acgctcacct ccacccgcac 972
 ccggttgcgc gtgtcagtgg ccaccgcg accgccccaa ggcgtgtcat cgggcacggt 1032
 tggttctgtt tcttcaatga tctgtggcgc ttccaccttg tttgtcatgg cgtcttcgc 1092
 tgccatgacg gcaaaccata acaggtAAC gatgccaccc cagcgcataa tatcgagcac 1152
 gatggcgcg gcattggaca aaagatcaac gccaaagggtg ccggcgatga aaaaaagac 1212
 gtcagaaatt aaacacacga gaagaaccgc aatgagtcct tcgcgtttaa ttccttg 1272
 aatcaccagt acattctgcg gtccgatgga cagtaaaaga ctggccccca aaagcagacc 1332
 tgtaatgaag atttccatga tcaccatcgt gacctatgga agtacttaag taaaatgatt 1392
 gggtcttaac atggtttaat atagcttc atg aac ccc att caa ctg gac act 1444
 Met Asn Pro Ile Gln Leu Asp Thr
 220 225
 ttg ctc tca atc att gat gaa ggc agc ttc gaa ggc gcc tcc tta gcc 1492
 Leu Leu Ser Ile Ile Asp Glu Gly Ser Phe Glu Gly Ala Ser Leu Ala
 230 235 240
 ctt tcc att tcc ccc tcg gcg gtg agt cag cgc gtt aaa gct ctc gag 1540
 Leu Ser Ile Ser Pro Ser Ala Val Ser Gln Arg Val Lys Ala Leu Glu
 245 250 255
 cat cac gtg ggt cga gtg ttg gta tcg cgc acc caa ccg gcc aaa gca 158
 His His Val Gly Arg Val Leu Val Ser Arg Thr Gln Pro Ala Lys Ala
 260 265 270

Seq_listing_us_korrigiert141102.txt

acc gaa gca gca ggt gaa gtc ctt gtg caa gca gca gca ggg aaa atg gtg ttg	1636
Thr Glu Ala Gly Glu Val Leu Val Gln Ala Ala Arg Lys Met Val Leu	
275 280 285	
ctg caa gca gaa act aaa gca caa cta tct gga cgc ctt gct gaa atc	1684
Leu Gln Ala Glu Thr Lys Ala Gln Leu Ser Gly Arg Leu Ala Glu Ile	
290 295 300 305	
ccg tta acc atc gcc atc aac gca gat tcg cta tcc aca tgg ttt cct	1732
Pro Leu Thr Ile Ala Ile Asn Ala Asp Ser Leu Ser Thr Trp Phe Pro	
310 315 320	
ccc gtg ttc aac gag gta gct tct tgg ggt gga gca acg ctc acg ctg	1780
Pro Val Phe Asn Glu Val Ala Ser Trp Gly Gly Ala Thr Leu Thr Leu	
325 330 335	
cgc ttg gaa gat gaa gca gac aca tta tcc ttg ctg cgg cgt gga gat	1828
Arg Leu Glu Asp Glu Ala His Thr Leu Ser Leu Leu Arg Arg Gly Asp	
340 345 350	
gtt tta gga gca gta acc cgt gaa gct aat ccc gtg gca gga tgg gaa	1876
Val Leu Gly Ala Val Thr Arg Glu Ala Asn Pro Val Ala Gly Cys Glu	
355 360 365	
gta gta gaa ctt gga acc atg cgc cac ttg gcc att gca acc ccc tca	1924
Val Val Glu Leu Gly Thr Met Arg His Leu Ala Ile Ala Thr Pro Ser	
370 375 380 385	
ttg cgg gat gcc tac atg gtt gat ggg aaa cta gat tgg gct gca atg	1972
Leu Arg Asp Ala Tyr Met Val Asp Gly Lys Leu Asp Trp Ala Ala Met	
390 395 400	
ccc gtc tta cgc ttc ggt ccc aaa gat gtg ctt caa gac cgt gac ctg	2020
Pro Val Leu Arg Phe Gly Pro Lys Asp Val Leu Gln Asp Arg Asp Leu	
405 410 415	
gac ggg cgc gtc gat ggt cct gtg ggg cgc agg cgc gta tcc att gtc	2068
Asp Gly Arg Val Asp Gly Pro Val Gly Arg Arg Arg Val Ser Ile Val	
420 425 430	
ccg tcg gca gaa ggt ttt ggt gag gca att cgc cga ggc ctt ggt tgg	2116
Pro Ser Ala Glu Gly Phe Gly Glu Ala Ile Arg Arg Gly Leu Gly Trp	
435 440 445	
gga ctt ctt ccc gaa acc caa gct gct ccc atg cta aaa gca gga gaa	2164
Gly Leu Leu Pro Glu Thr Gln Ala Ala Pro Met Leu Lys Ala Gly Glu	
450 455 460 465	
gtg atc ctc ctc gat gag ata ccc att gac aca ccg atg tat tgg caa	2212
Val Ile Leu Leu Asp Glu Ile Pro Ile Asp Thr Pro Met Tyr Trp Gln	
470 475 480	
cga tgg cgc ctg gaa tct aga tct cta gct aga ctc aca gac gcc gtc	2260
Arg Trp Arg Leu Glu Ser Arg Ser Leu Ala Arg Leu Thr Asp Ala Val	
485 490 495	
gtt gat gca gca atc gag gga ttg cgg cct tag ttacttctga aaaggttcag	2313
Val Asp Ala Ala Ile Glu Gly Leu Arg Pro	
500 505	
ggttttcac ttcttcgccc gcaggaattt ggccaggcag agtaaacacct tcagcaaatg	2373
g	2374

Seq_listing_US_korrigiert141102.txt

<210> 4
<211> 216
<212> PRT
<213> Corynebacterium glutamicum
<220> (orf3)

<400> 4
Asp Thr Pro Leu Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile Val Ala
1 5 10 15
Ser Gly Lys Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu Leu
20 25 30
Thr Ala Glu Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu Leu
35 40 45
Ile His Gln Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu Pro
50 55 60
Gly Asp Asp Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly Leu
65 70 75 80
Gly Val Ile Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp Lys
85 90 95
Tyr Leu Asp Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys Ser
100 105 110
Leu Ser Glu Gly Met Leu Asn Val Asn Asn Ile Asp Met Val Arg Lys
115 120 125
Leu Asn Asp Ile Ala Gln Glu Arg Gly Gln Ser Leu Ala Gln Met Ala
130 135 140
Leu Ala Trp Val Leu Arg Glu Gln Gly Glu Tyr Gly Ala Asp Thr Val
145 150 155 160
Thr Ser Ala Leu Ile Gly Ala Ser Ser Val Glu Gln Leu Asp Asn Ser
165 170 175
Leu Asp Ser Leu Asn Asn Leu Glu Phe Ser Asp Ala Glu Leu Glu Ala
180 185 190
Ile Asp Glu Ile Ser His Asp Ala Gly Ile Asn Ile Trp Ala Lys Ala
195 200 205
Thr Asp Ser Lys Thr Arg Glu Asn
210 215

<210> 5
<211> 290
<212> PRT
<213> Corynebacterium glutamicum
<220> (LysG)

<400> 5
Met Asn Pro Ile Gln Leu Asp Thr Leu Leu Ser Ile Ile Asp Glu Gly
1 5 10 15
Ser Phe Glu Gly Ala Ser Leu Ala Leu Ser Ile Ser Pro Ser Ala Val

Seq_listing_us_korrigiert141102.txt
25 30

Ser Gln Arg Val Lys Ala Leu Glu His His Val Gly Arg Val Leu Val
 35 40 45

Ser Arg Thr Gln Pro Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val
 50 55 60

Gln Ala Ala Arg Lys Met Val Leu Leu Gln Ala Glu Thr Lys Ala Gln
 65 70 75 80

Leu Ser Gly Arg Leu Ala Glu Ile Pro Leu Thr Ile Ala Ile Asn Ala
 85 90 95

Asp Ser Leu Ser Thr Trp Phe Pro Pro Val Phe Asn Glu Val Ala Ser
 100 105 110

Trp Gly Gly Ala Thr Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr
 115 120 125

Leu Ser Leu Leu Arg Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu
 130 135 140

Ala Asn Pro Val Ala Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg
 145 150 155 160

His Leu Ala Ile Ala Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp
 165 170 175

Gly Lys Leu Asp Trp Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys
 180 185 190

Asp Val Leu Gln Asp Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val
 195 200 205

Gly Arg Arg Arg Val Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu
 210 215 220

Ala Ile Arg Arg Gly Leu Gly Trp Gly Leu Leu Pro Glu Thr Gln Ala
 225 230 235 240

Ala Pro Met Leu Lys Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro
 245 250 255

Ile Asp Thr Pro Met Tyr Trp Gln Arg Trp Arg Leu Glu Ser Arg Ser
 260 265 270

Leu Ala Arg Leu Thr Asp Ala Val Val Asp Ala Ala Ile Glu Gly Leu
 275 280 285

Arg Pro
 290

FZJ 9910 PCT/US 8/8 12.11.02
US 09/105,117